

START 2
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 TCCGGGAGCTGCACGGGGCTGCGTGGAAGAGCGCCGAGCGGTGGCGTCTGTGCGCCCCCTCTCGTGGGAAGAATC
 START SEQ ID# 2
 GTTTGGTCTCCTGCGGTGCCCGGAATCCAGTCAGAAGTCCAGCCTGCCACTGTTCTCTGATGCCA CCA GCA 3
 START SEQ ID# 3
 P T Q L F F P L I R N C E L S R I Y G T 9
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 A C Y C H H K H L C C S S S Y I P Q S R 43
 GCA TGT TAC TGC CAC CAC AAA CAT CTC TGT TGT TCC TCA TCG TAC ATT CCT CAG AGT CGA 129
 L R Y T P H P A Y A T F C R P K E N W W 63
 CTG AGA TAC ACA CCT CAT CCA GCA TAT GCT ACC TTT TGC AGG CCA AAG GAG AAC TGG TGG 189
 Q Y T Q G R R Y A S T P Q K F Y L T P P 83
 CAG TAC ACC CAA GGA AGG AGA TAT GCT TCC ACA CCA CAG AAA TTT TAC CTC ACA CCT CCA 249
 Q V N S I L K A N E Y S F K V P E F D G 103
 CAA GTC AAT AGC ATC CTT AAA GCT AAT GAA TAC AGT TTC AAA GTG CCA GAA TTT GAC GGC 309
 K N V S S I L G F D S N Q L P A N A P I 123
 AAA AAT GTC AGT TCT ATC CTT GGA TTT GAC AGC AAT CAG CTG CCT GCA AAT GCA CCC ATT 369
 E D R R S A A T C L Q T R G M L L G V F 143
 GAG GAC CGG AGA AGT GCA GCA ACC TGC TTG CAG ACC AGA GGG ATG CTT TTG GGG GTT TTT 429
 D G H A G C A C S Q A V S E R L F Y Y I 163
 GAT GGC CAT GCA GGT TGT GCT TGT TCC CAG GCA GTC AGT GAA AGA CTC TTT TAT TAT ATT 489
 A V S L L P H E T L L E I E N A V E S G 183
 GCT GTC TCT TTG TTA CCC CAT GAG ACT TTG CTA GAG ATT GAA AAT GCA GTG GAG AGC GGC 549
 R A L L P I L Q W H K H P N D Y F S K E 203
 CGG GCA CTG CTA CCC ATT CTC CAG TGG CAC AAG CAC CCC AAT GAT TAC TTT AGT AAG GAG 609
 A S K L Y F N S L R T Y W Q E L I D L N 223
 GCA TCC AAA TTG TAC TTT AAC AGC TTG AGG ACT TAC TGG CAA GAG CTT ATA GAC CTC AAC 669
 T G E S T D I D V K E A L I N A F K R L 243
 ACT GGT GAG TCG ACT GAT ATT GAT GTT AAG GAG GCT CTA ATT AAT GCC TTC AAG AGG CTT 729
 D N D I S L E A Q V G D P N S F L N Y L 263
 GAT AAT GAC ATC TCC TTG GAG GCG CAA GTT GGT GAT CCT AAT TCT TTT CTC AAC TAC CTG 789
 V L R V A F S G A T A C V A H V D G V D 283
 GTG CTT CGA GTG GCA TTT TCT GGA GCC ACT GCT TGT GTG GCC CAT GTG GAT GGT GTT GAC 849
 L H V A N T G D S R A M L G V Q E E D G 303
 CTT CAT GTG GCC AAT ACT GGC GAT AGC AGA GCC ATG CTG GGT GTG CAG GAA GAG GAC GGC 909

Figure 1A

S W S A V T L S D H N A Q N E R E L E 323
 TCA TGG TCA GCA GTC ACG CTG TCT AAT GAC CAC AAT GCT CAA AAT GAA AGA GAA CTA GAA 969

 R L K L E H P K S E A K S V V K Q D R L 343
 CGG CTG AAA TTG GAA CAT CCA AAG AGT GAG GCC AAG AGT GTC GTG AAA CAG GAT CGG CTG 1029

 L G L L M P F R A F G D V K F K W S I D 363
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 L Q K R V I E S G P D Q L N D N E Y T K 383
 CTT CAA AAG AGA GTG ATA GAA TCT GGC CCA GAC CAG TTG AAT GAC AAT GAA TAT ACC AAG 1149

 F I P P N Y H T P P Y L T A E P E V T Y 403
 TTT ATT CCT CCT AAT TAT CAC ACA CCT CCT TAT CTC ACT GCT GAG CCA GAG GTA ACT TAC 1209

 H R L R P Q D K F L V L A T D G L W E T 423
 CAC CGA TTA AGG CCA CAG GAT AAG TTT CTG GTG TTG GCT ACT GAT GGG TTG TGG GAG ACT 1269

 M H R Q D V V R I V G E Y L T G M H H Q 443
 ATG CAT AGG CAG GAT GTG GTT AGG ATT GTG GGT GAG TAC CTA ACT GGC ATG CAT CAC CAA 1329

 Q P I A V G G Y K V T L G Q M H G L L T 463
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 E R R T K M S S V F E D Q N A A T H L I 483
 GAA AGG AGA ACC AAA ATG TCC TCG GTA TTT GAG GAT CAG AAC GCA GCA ACC CAT CTC ATT 1449

 R H A V G N N E F G T V D H E R L S K M 503
 CGC CAC GCT GTG GGC AAC AAC GAG TTT GGG ACT GTT GAT CAT GAG CGC CTC TCT AAA ATG 1509

 L S L P E E L A R M Y R D D I T I I V V 523
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End of seq IDNO: 2
 End of seq IDNO: 3
 End of seq IDNO: 1

Figure 1.B

Analysis of 26583 (537 aa)

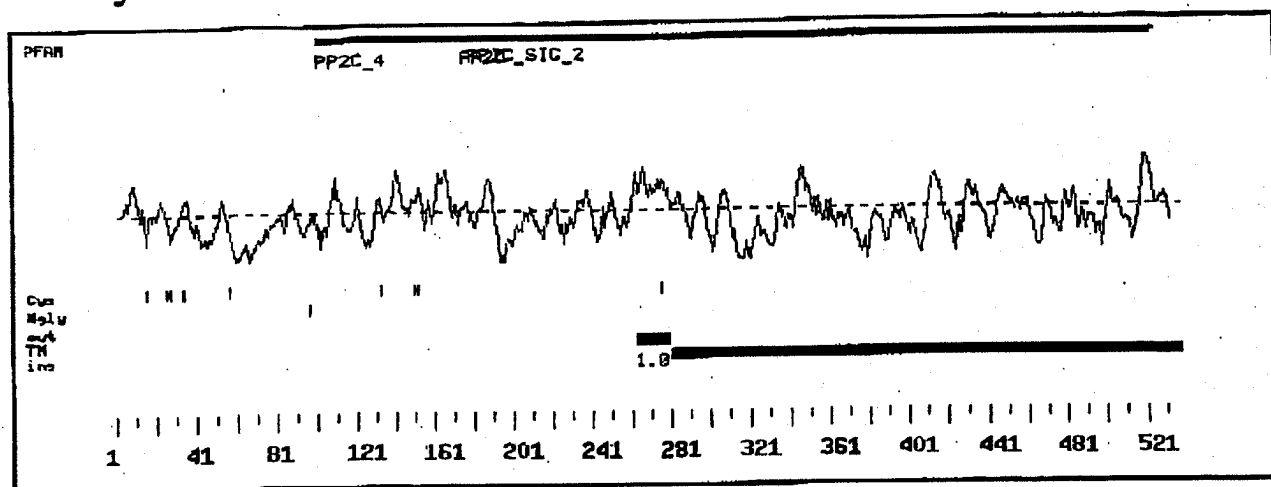


Figure 2

PP2C: domain 1 of 1, from 173 to 461: score 261.3, E = 1.3e-74

```

-->ldvgyvzmqgwrkamepahialkninsgkdwaffavfDChgGs
1 **** + F *** +++++ ** s++ s+ *f *** +
26583 173 LLEIENAVESGRALLPILOWHKHHPNDYF-SKEASKLYFNSLRTYWQE 218 SEQ ID NO:2

qaakyagkhkhk.tilaerksfpegdpwEmklsdledalkesfleadtde
+ *g++ *** + a++ f+ +d+ d + **** +++++
26583 219 LIDLNTGESTDIdVKEALINAFKRLDN-----DISLEAQVGDPNSFLNY 262

elrsaaasaankvltkedlssGstAvvalirgnkLyVANvGDSravLcrn
*** + SC+TA+va++g +L+VAN+GDSRa+L+ +
26583 263 LVLR-----VAFSGATACVAHVdGVdLHVANTGDSRAHLGVQ 299

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26583 300 EEDGSW=AVTLSNDHNAQNERELERLKLHHPKSEAKSvvkQDRLLGLLMP 349

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26583 350 FRAFGDVkPKWSIDLQKRViesGpDQLNDnERTKFiPPnyhtpPYLTAEF 399

dvtssdtltpdkDefliLacDGLWDvvsdqewvdivrsalsdgnksaedp
+vt +++l+p+ D+Fl+LA+DGLW++++ q+vv iv + l+ + +
26583 400 EVT-YHRLRPQ-DKFLVLATDGLWETMHRQDVVRIVGEYLTGM-----H 441

meaaeklvdaaiargseDni<-*
++ ++ + + g ++
26583 442 HQQPIAVGGYKVTLCQMHL 461

```

Figure 3A

00001057-030001

00001257-030607

```

PF2C_4: domain 1 of 1, from 99 to 523: score 338.5, E = 7.6e-98
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+ gkn +++ g+ +++++ p+ED+ ++ + +++++ + gVED
26583 99 PFIDGKNVSSILGF-DSNQLPANAPIEDRRSAATClqcrgmLLGVFD 144      SEQ ID NO:2

CHGGseasakflskniheilaeelsfdkdeslkene.e.lk.d.ep.....
GH+G ++++ +s+l+ +a +l +++ ++ an+ +++++ + + + + +
26583 145 GHACCACSQAVSERLFYYIAVSLPHETLLEIENAVEsGRaLiPiIqwhk 194

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++++ ++ + + + + + + + + + + + + + + + + + + + + + + + + +
26583 195 hndyfskaasklyfnsrlrtywqElIdLnTGESTDIDVKEALINAFKRLD 244

eei.....sTAvvalirgnklyvANvGDSRa
++i+ + + +++++ + + + + + + + + + + + + + + + + + + + + +
26583 245 NDisleaqvgdpnsflnylvrva fsgATACVAHVdGVdLHVANTGDSRA 294

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+L+ + +d+sw sav L++DK++ ne+E+eR++ +++++ + + + + +
26583 295 MLGVQEEDgSW-----SAVTLSDHNAQNRELERLKLKLEPKSE--AKS 336

fvsngggvrvvRvngvvisLavsRaiGdfelKk.ked.e.lie.....en.
+v ++ R++G L++ Ra+GD+++K+++++++ie++++++n+
26583 337 VVKQD-----RLGL---LMPFRAFGDVKFKWIDLqKrVIEsgpdqLNd 378

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26583 379 NEYTKFIFPNYHTFPYLTAEPVTYHRL-----RPQDKFLVLATDGLWE 422

visnqeavdivrkhlrkgddk.evksaaqela.r.a.d....s.....
+ q++v iv + l+++++++ +++++ +++++ +++++ +
26583 423 TTHRQDVVRIVGEYLTGPHGQPIAVGCKYVTlGqMNCilteRrtkmsv 472

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26583 473 fedqnaathLirhavGNNEFGTVdHERLSKMLsipeelarwyADOITIV 522

v<-?
v
26583 523 V 523

```

Figure 3B

26583 Expression in Clinical Tissue Samples

